

## 102769.TXT

## SEQUENCE LISTING

&lt;110&gt; Karo Bio AB

<120> CRYSTALLINE LIVER X RECEPTOR BETA  
PROTEIN

&lt;130&gt; 102769

&lt;140&gt; 10/540,612

&lt;141&gt; 2005-06-23

&lt;150&gt; PCT/IB2003/006412

&lt;151&gt; 2003-12-24

&lt;150&gt; GB 0230177.8

&lt;151&gt; 2002-12-24

&lt;160&gt; 2

&lt;170&gt; FastSEQ for windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

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Met Ser Ser Pro Thr Thr Ser Ser Leu Asp Thr Pro Leu Pro Gly Asn
 1      5      10      15
Gly Pro Pro Gln Pro Gly Ala Pro Ser Ser Ser Pro Thr Val Lys Glu
      20      25      30
Glu Gly Pro Glu Pro Trp Pro Gly Pro Asp Pro Asp Val Pro Gly
      35      40      45
Thr Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp
      50      55      60
Pro Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys
65      70      75      80
Met Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly
      85      90      95
Phe His Tyr Asn Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg
      100      105      110
Arg Ser Val Val Arg Gly Gly Ala Arg Arg Tyr Ala Cys Arg Gly Gly
      115      120      125
Gly Thr Cys Gln Met Asp Ala Phe Met Arg Arg Lys Cys Gln Gln Cys
      130      135      140
Arg Leu Arg Lys Cys Lys Glu Ala Gly Met Arg Glu Gln Cys Val Leu
145      150      155      160
Ser Glu Glu Gln Ile Arg Lys Lys Lys Ile Arg Lys Gln Gln Gln Gln
      165      170      175
Glu Ser Gln Ser Gln Ser Pro Val Gly Pro Gln Gly Ser Ser
      180      185      190
Ser Ser Ala Ser Gly Pro Gly Ala Ser Pro Gly Gly Ser Glu Ala Gly
      195      200      205
Ser Gln Gly Ser Gly Glu Gly Glu Gly Val Gln Leu Thr Ala Ala Gln
210      215      220
Glu Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn Lys
225      230      235      240
Arg Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly Ala
      245      250      255
Asp Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe Thr
      260      265      270

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Glu	Leu	Ala	Ile	Ile	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln
		275					280					285			
Val	Pro	Gly	Phe	Leu	Gln	Leu	Gly	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu
	290					295					300				
Lys	Ala	Ser	Thr	Ile	Glu	Ile	Met	Leu	Leu	Glu	Thr	Ala	Arg	Arg	Tyr
305					310					315					320
Asn	His	Glu	Thr	Glu	Cys	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Thr	Tyr	Ser
				325						330				335	
Lys	Asp	Asp	Phe	His	Arg	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro
			340					345					350		
Ile	Phe	Glu	Phe	Ser	Arg	Ala	Met	Arg	Arg	Leu	Gly	Leu	Asp	Asp	Ala
		355					360					365			
Glu	Tyr	Ala	Leu	Leu	Ile	Ala	Ile	Asn	Ile	Phe	Ser	Ala	Asp	Arg	Pro
	370					375					380				
Asn	Val	Gln	Glu	Pro	Gly	Arg	Val	Glu	Ala	Leu	Gln	Gln	Pro	Tyr	Val
385					390					395					400
Glu	Ala	Leu	Leu	Ser	Tyr	Thr	Arg	Ile	Lys	Arg	Pro	Gln	Asp	Gln	Leu
				405					410					415	
Arg	Phe	Pro	Arg	Met	Leu	Met	Lys	Leu	Val	Ser	Leu	Arg	Thr	Leu	Ser
			420					425					430		
Ser	Val	His	Ser	Glu	Gln	Val	Phe	Ala	Leu	Arg	Leu	Gln	Asp	Lys	Lys
		435					440					445			
Leu	Pro	Pro	Leu	Leu	Ser	Glu	Ile	Trp	Asp	Val	His	Glu			
	450					455					460				

<210> 2

<211> 208

<212> PRT

<213> Artificial Sequence

<220>

<223> The crytallised protein sequence with the first four non-LXR Beta amino acid residues (GSHM) fused to the N-terminal end of residues 213-416 originating from human LXR Beta

<400> 2

Gly	Ser	His	Met	Gly	Glu	Gly	Glu	Gly	Val	Gln	Leu	Thr	Ala	Ala	Gln
1				5					10					15	
Glu	Leu	Met	Ile	Gln	Gln	Leu	Val	Ala	Ala	Gln	Leu	Gln	Cys	Asn	Lys
			20					25					30		
Arg	Ser	Phe	Ser	Asp	Gln	Pro	Lys	Val	Thr	Pro	Trp	Pro	Leu	Gly	Ala
		35					40					45			
Asp	Pro	Gln	Ser	Arg	Asp	Ala	Arg	Gln	Gln	Arg	Phe	Ala	His	Phe	Thr
	50					55					60				
Glu	Leu	Ala	Ile	Ile	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln
65					70					75					80
Val	Pro	Gly	Phe	Leu	Gln	Leu	Gly	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu
			85						90					95	
Lys	Ala	Ser	Thr	Ile	Glu	Ile	Met	Leu	Leu	Glu	Thr	Ala	Arg	Arg	Tyr
			100					105					110		
Asn	His	Glu	Thr	Glu	Cys	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Thr	Tyr	Ser
		115					120					125			
Lys	Asp	Asp	Phe	His	Arg	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro
	130					135					140				
Ile	Phe	Glu	Phe	Ser	Arg	Ala	Met	Arg	Arg	Leu	Gly	Leu	Asp	Asp	Ala
145					150					155					160
Glu	Tyr	Ala	Leu	Leu	Ile	Ala	Ile	Asn	Ile	Phe	Ser	Ala	Asp	Arg	Pro
			165					170						175	
Asn	Val	Gln	Glu	Pro	Gly	Arg	Val	Glu	Ala	Leu	Gln	Gln	Pro	Tyr	Val
		180						185					190		
Glu	Ala	Leu	Leu	Ser	Tyr	Thr	Arg	Ile	Lys	Arg	Pro	Gln	Asp	Gln	Leu

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